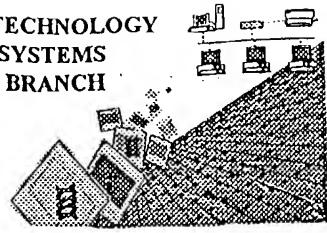# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/814,760_

Source: _IFWO_

Date Processed by STIC: _9/24/04_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04): U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/814,760_

1____Wrapped Nucleics / Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3____Misaligned Amino Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4____Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5____Variable Length Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____Skipped Sequences (OLD RULES) Sequence(s)____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences (NEW RULES) Sequence(s)_____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n/Xaa "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

Please consult Sequence Rules for valid format

Also, see item 4 on Error Summary Sheet, and item 2 on Error Summary Sheet IFWO

delete extra <110's; show <110 only once

RAW SEQUENCE LISTING DATE: 09/24/2004
PATENT APPLICATION: US/10/814,760 TIME: 10:49:45

pp 2-4

Input Set : N:\LMOORE\PTO.LM.txt
Output Set: N:\CRF4\09242004\J814760.raw

Does Not Comply Corrected Diskette Needed

```
8  <110> APPLICANT: Buchanan, F.
```
W--> 4 <110> APPLICANT: Thue, T.D.
W--> 5 <110> APPLICANT: Winkelman-Sim, D.
W--> 6 <120> TITLE OF INVENTION: CRH and POMC Effects on Animal Growth
W--> 7 <130> FILE REFERENCE: 1696-04-02
C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/814,760
C--> 8 <141> CURRENT FILING DATE: 2004-03-31
E--> 9 <160> NUMBER OF SEQ ID NOS: Number of SEQ ID NOS: 9
```
    10 <170> SOFTWARE: Microsoft Office 2004; Windows XP Professional O/S.
```

see P.2 for explanation of global error

ERRORED SEQUENCES

E--> 13 <210> SEQ ID NO: SEQ ID NO: 1
```
    14 <211> LENGTH: LENGTH: 584 base pairs
```
E--> 15 <212> TYPE: TYPE: DNA
```
    16 <213> ORGANISM: ORGANISM: Bos taurus
```
W--> 17 <220> FEATURE: FEATURE: SNPs present at nucleotides 22 ("CRH4"), 145 ("CRH45") and 240
W--> 18 ("CRH77").
```
    19 <223> OTHER INFORMATION: OTHER INFORMATION: GenBank Accession AF340152
```
E--> 21 <400> SEQUENCE: SEQUENCE 1
W--> 22 1   cgcccgctaa aatgcgactg ccgctgctcg tgtccgtggg cgtcctgctg gtggctctgc
W--> 23 61 tgccctcccc gccatgcagg gccctcctca gccggggggcc catcccgggt gcccggcagg
W--> 24 121 catcacagca cccccagccc ctgagtttct tccagccgcc gccgcagccc caggaacccc
W--> 25 181 aggctctgcc caccctactc cgtgttgggg aggaatactt cctccgcctg ggtaacctcg
W--> 26 241 atgagacccg ggctgctccs ctctctcccg ccgcctcgcc tctcgccagc agaagcagca
W--> 27 301 gtcgcctttc tccggacaag gtggccgcca acttttttccg agcgctgctg cagccccggc
W--> 28 361 gcccattcga cagcccagcg ggtcccgcgg aacgcggcac ggagaacgcc ctcggcagcc
W--> 29 421 gccaggaggc gccggccgcc aggaagaggc gatcccagga acctcccatc tccctggatc
W--> 30 481 tcaccttcca cctcctccga gaagtcttgg aaatgaccaa ggccgatcag ttagcacagc
E--> 31 541 aagctcatar caayaggaaa ctgttggaca ttgctgggaa atga
E--> 35 <210> SEQ ID NO: SEQ ID NO: 2
```
    36 <211> LENGTH: LENGTH: 1002 base pairs
```
E--> 37 <212> TYPE: TYPE: DNA
```
    38 <213> ORGANISM: ORGANISM: Bos taurus
```
W--> 39 <220> FEATURE: FEATURE: SNP at position 254
```
    40 <223> OTHER INFORMATION: OTHER INFORMATION: GenBank Accession J00021
```
E--> 42 <400> SEQUENCE: SEQUENCE 2
W--> 43 1   gcggagggag tggaaggctc aggcggcgcg cttgaggggc gggtgaacgc cgcggcctgg
W--> 44 61 agtgggcggg gcctgacgcg ctctgccgct ctccgcaggc gtgcatccgg gcctgcaagc
W--> 45 121 ccgacctctc cgccgagacg ccggtgttcc ccggcaacgg cgatgagcag ccgctgactg
W--> 46 181 agaaccccccg gaagtacgtc atgggccatt tccgctggga ccgcttcggc cgtcggaatg
W--> 47 241 gtagcagcag cagcggagtt gggggcgcgg cccagaagcg cgaggaggaa gtggcggtgg

Sequence Listing

<110> Buchanan, F.
<110> Thue, T.D.
<110> Winkelman-Sim, D.
<120> CRH and POMC Effects on Animal Growth
<130> 1696-04-02
<141> March 31, 2004
<160> Number of SEQ ID NOS: 9
<170> Microsoft Office 2004; Windows XP Professional O/S.

<210> SEQ ID NO: 1
<211> LENGTH: 584 base pairs
<212> TYPE: DNA
<213> ORGANISM: Bos taurus
<220> FEATURE: SNPs present at nucleotides 22 ("CRH4"), 145 ("CRH45") and 240 ("CRH77").
<223> OTHER INFORMATION: GenBank Accession AF340152

<400> SEQUENCE 1

```
1    cgcccgctaa aatgcgactg ccgctgctcg tgtccgtggg cgtcctgctg gtggctctgc    60
61   tgccctcccc gccatgcagg gccctcctca gccggggggcc catcccgggt gcccggcagg   120
121  catcacagca cccccagccc ctgagtttct tccagccgcc gccgcagccc caggaacccc   180
181  aggctctgcc caccctactc cgtgttgggg aggaatactt cctccgcctg ggtaacctcg
241  atgagacccg ggctgctccs ctctctcccg ccgcctcgcc tctcgccagc agaagcagca
301  gtcgcctttc tccggacaag gtggccgcca acttttccg agcgctgctg cagccccggc
361  gcccattcga cagcccagcg ggtcccgcgg aacgcggcac ggagaacgcc ctcggcagcc
421  gccaggaggc gccggccgcc aggaagaggc gatcccagga acctcccatc tccctggatc
481  tcaccttcca cctcctccga gaagtcttgg aaatgaccaa ggccgatcag ttagcacagc
541  aagctcatar caayaggaaa ctgttggaca ttgctgggaa atga
```

[Handwritten annotations throughout:]

Delete (next to the three <110> lines)

<140> 10/814,760 <—insert

do not insert alphabetical headings   2004-03-31   use this format for dates

Delete alphabetical headings

do not insert ANY response to <220>. It is a header only.

move to <2237 line

<3007 <
<3087 <
<3097 <— insert w/response

60, 120, 180 — insert cumulative nucleotide totals at right margin of each line.

Delete

The above sequence shows samples of global errors.

see pp. 3-4 for more errors

Move any explanatory material to <2237 line.

Also, do not insert database accession number on <2237 line. It belongs in <3007 section. Insert <3007 with no response. It is a header only. Insert <3087 and accession number. Insert <3097 and response.

(See 1.823 of Sequence Rules for valid format.)

```
<210>  SEQ ID NO:      3
<211>  LENGTH:         1809 base pairs
<212>  TYPE:           DNA
<213>  ORGANISM:       Bos taurus
<223>  FEATURE:        SNP at position 1069
<223>  OTHER INFORMATION:  Genbank Accession No. AF265221
<400>  SEQUENCE 3
N      cagcctaaga tttccaagtg atgctgacca gagccacact tgaaagagac tgaaaacttc   60
61     ctttccagct ccggagcatg ggacatttat tcacagcagg catgccactc tccgccgcct  120
121    aactttcgtt tggggcaagt caagactgga gaaaggtgct gaggctgcca gatccaggag  180
```

insert

<2207

goes on <223> line   goes on <3087 line

insert

<300> ← no response
<308> ←
<309> ← insert response

(partial listing of sequence 3)

The above is a sample of global error.

```
        <210>  SEQ ID NO:   6
        <211>  LENGTH:      21
        <212>  TYPE:        DNA
        <213>  ORGANISM:    Bos taurus          insert <2207 above <2237
2207 (  <2237 (>223>) OTHER-INFORMATION:  Forward primer for DNA amplification of sequences
        within SEQ ID NO: 2.

use
forward <400>  SEQUENCE  6
bracket    1    cgtgcatccg ggcctgcaag c 21
```

The above is another sample of global error.

Please see sample Sequence Listing
(attached) for valid format.

```
<110>        Smith, John;  Smithgene Inc.

<120>        Example of a Sequence Listing

<130>        01-00001

<140>        PCT/EP98/00001
<141>        1998-12-31

<150>        US 08/999,999
<151>        1997-10-15

<160>        4

<170>        PatentIn version 2.0

<210>        1
<211>        389
<212>        DNA
<213>        Paramecium sp.

<220>
<221>        CDS
<222>        (279)...(389)

<300>
<301>        Doe, Richard
<302>        Isolation and Characterization of a Gene Encoding a
             Protease from Paramecium sp.
<303>        Journal of Genes
<304>        1
<305>        4
<306>        1-7
<307>        1988-06-31
<308>        123456
<309>        1988-06-31

<400>        1
agctgtagtc  attcctgtgt  cctcttctct  ctgggcttct  caccctgcta  atcagatctc        60

agggagagtg  tcttgaccct  cctctgcctt  tgcagcttca  caggcaggca  ggcaggcagc       120

tgatgtggca  attgctggca  gtgccacagg  cttttcagcc  aggcttaggg  tgggttccgc       180

cgcggcgcgg  cggcccctct  cgcgctcctc  tcgcgcctct  ctctcgctct  cctctcgctc       240
```

Consult this (handwritten)

										atg	gtt	tca	atg	ttc	agc	296
ggacctgatt			aggtgagcag			gaggagggggg			cagttagc	Met	Val	Ser	Met	Phe	Ser	
										1				5		

ttg	tct	ttc	aaa	tgg	cct	gga	ttt	tgt	ttg	ttt	gtt	tgt	ttg	ttc	caa	344
Leu	Ser	Phe	Lys	Trp	Pro	Gly	Phe	Cys	Leu	Phe	Val	Cys	Leu	Phe	Gln	
			10					15					20			

tgt	ccc	aaa	gtc	ctc	ccc	tgt	cac	tca	tca	ctg	cag	ccg	aat	ctt		389
Cys	Pro	Lys	Val	Leu	Pro	Cys	His	Ser	Ser	Leu	Gln	Pro	Asn	Leu		
		25					30					35				

```
<210>        2
<211>        37
<212>        PRT
<213>        Paramecium sp.
```

```
<400>        2
```

Met	Val	Ser	Met	Phe	Ser	Leu	Ser	Phe	Lys	Trp	Pro	Gly	Phe	Cys	Leu
1				5					10					15	

Phe	Val	Cys	Leu	Phe	Gln	Cys	Pro	Lys	Val	Leu	Pro	Cys	His	Ser	Ser
			20					25					30		

Leu	Gln	Pro	Asn	Leu
		35		

```
<210>        3
<211>        11
<212>        PRT
<213>        Artificial Sequence
```

```
<220>
<223>        Designed peptide based on size and polarity to act as a
             linker between the alpha and beta chains of Protein XYZ.
```

```
<400>        3
```

Met	Val	Asn	Leu	Glu	Pro	Met	His	Thr	Glu	Ile
1				5					10	

```
<210>        4
<400>        4
000
```

[Annex VIII follows]